Form 1449 (Modified)

Atty Docket No. MXGNP004X1/0311.310

Application No.:

Applicant: July 29, 2003

Other Documents

10/629,351

Gustafsson et al. Filing Date

Group 1645

(Use Several Sheets if Necessary)

Information Disclosure

Statement By Applicant

		Other Documents
Examiner		
Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Hellberg et al., "The Prediction of Bradykinin Potentiating Potency of
		Pentapeptides. An Example of a Peptide Quantitative Structure-Activity
		Relationship," Acia Chemica Scandinaviea B 40, pp. 135-140, 1988
	C2	Bucht et al., "Optimising the Signal Peptide for Glycosyl Phosphatidylinositol
		Modification of Human Acetylcholinesterase Using Mutational Analysis and
		Peptide-Quantitative Structure-Activity Relationships," Biochimica et
		Biophysica Acta 1431, pp. 471-482, 1999
	C3	Sandberg et al., "Engineering Multiple Properties of a Protein by
		Combinatorial Mutagenesis," Proc. Natl. Acad. Sci. USA, Vol. 90, pp. 8367-
		8371, September 1993
	C4	Wrede et al., "Peptide Design Aided by Neural Networks: Biological Activity
		of Artificial Signal Peptidase I Cleavage Sites," Biochemistry, 37, pp. 3588-
		3593, 1998
	C5	Jill Damborsky, "Quantitative Structure-Function and Structure-Stability
	1	Relationships of Purposely Modified Proteins," Protein Engineering, Vol. 11,
		no. 1, pp. 21-30, 1998
	C6	Hellberg, et al., "Peptide Quantitative Structure-Activity Relationships, a
		Multivariate Approach," J. Med Chem, 30: pp 1126-1195, 1987
	C7	Sandberg et al., "New Chemical Descriptors Relevant for the Design of
	ł	Biologically Active Peptides. A Multivariate Characterization of 87 Amino
	l	Acids," J. Med Chem., 41, pp. 2481-2491, 1998
	C8	Casari et al., "A Method to Predict Functional Residues in Proteins," Nat.
		Struct Biol., 2, pp. 171-178, 1995
	C9	Suzuki et al., "A Method for Detecting Positive Selection at Single Amino
		Acid Sites," Mol. Biol. Evol. 16 (10): pp. 1315-1328, 1999
	C10	
	1	Divergent Evolution of Protein Sequences," Protein Engineering, Vol. 7, No.
		11, pp. 1323-1332, 1994
	1	

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure Statement By Applicant	Applicant: Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

_ C1	
	Groups in Databases of Protein Families," Proc. Int. Conf. Intell. Syst. Mol.
	Biol., 4, pp. 230-240, 1996
C12	
	Automated Mutation Strategy to Design Peptides and Pseudopeptides from
	Substitution Matrices," Journal of Molecular Graphics and Modelling, 17, pp.
	292-309, 1999
C1:	
	Some Substance P-Related Peptides," J. Peptide Res., 49, pp. 155-162, 1997
C14	
	Thesis, Umea: Umea University, 78 pages, 1997
C1:	
	Bradykinins Containing L-and D-Amino Acids," Acta Chemica Scandinavica,
	44, pp. 50-56, 1990
C10	
	Bradykinin-Potentiating Peptides," European Journal of Pharmacology, 79,
	pp. 155-158, 1982
C1	
	Escherichia Coli," Symposium Series No. 7, pp. 365-376, 1980
CI	
	Simplifying Protein Engineering," Proc. Natl. Acad. Sci., Vol. 93, pp. 10753-
	10757, 1996
C19	
	and Empirical Pair Score Functions," J. Mol. Biol., 255, pp. 641-665, 1996
C20	
	Sweden: University of Umea: 1986
C2	
	Ribonuclease S Protein," Science, 223: 1299-1301, 1984
C2:	
	Directed Evolution," Biotechnol. Prog, 15: 467-471, 1999
C2:	
	Interaction Preference is NP-Complete," Protein Eng., 7:1059-1068, 1994
C24	
	Using Ribosomes Display," Proc. Natl. Acad. Sci. USA, 94: 4937-4942, 1997
C2:	
	vitro," Curr Opin Biotechnol, 3:355-362, 1992

Pg. 2 of 8

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure	Applicant:	
Statement By Applicant	Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

C26	Johnson et al., "The Traveling Salesman Problem: A Case Study in Local Optimization," In Local Search in Combinatorial Optimization, Edited by Aarts et al., John Wiley & Sons Ltd., 21-310, 1997
C28	Jonsson et al., "Quantitative Sequence-Activity Models (QSAM) – Tools for Sequence Design," Nucleic Acids Res., 21:733-739, 1993
C29	Geladi et al., "Partial Least Squares Regression: A Tutorial," Anal Chim Acta, 168: 1-17, 1986
C30	Holowachuk et al., "Efficient Gene Synthesis by Klenow Assembly/Extension-Pfu Polymerase Amplification (KAPPA) of Overlapping Olingonucleotides," PCR Methods Appl, 4:299-302, 1995
C31	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for Quantitative Structure-Activity Relationships," Int J Pept Protein Res, 37:414-424, 1991
C32	Mee et al., "Design of Active Analogues of a 15-Residue Peptide Using D- Optimal Design, QSAR and a Combinatorial Search Algorithm," J Pept Res, 49:89-102, 1997
C33	Schneider et al., "Peptide Design by Artificial Neural Networks and Compouter-Based Evolutionary Search," Proc Natl Acad Sci USA, 95:12179-12184, 1998
C34	Sjostrom et al.," Signal Peptide Amino Acid Sequences in Escharichla Coli Contain Information Related to Final Protein Localization, A Multivariate Data Analysis," EMBO, 6:823-891, 1987
C35	Patel et al., "Patenting Computer-Designed Peptides," Journal of Computer-Aided Molecular Design, 12:543-556, 1998
C36	Aita et al., "Theory of Evolutionary Molecular Engineering Through Simultaneous Accumulation of Advantageous Mutations," J. Theor. Biol., 207:543-556, 2000
C37	Darius et al., "Simulated Molecular Evolution of Computer Generated Artifacts?," Biophysical Journal, 67:2120-2122, 1994
C38	Singh et al., "Application of Genetic Algorithms to Combinatorial Synthesis: A Computational Approach to Lead Identification and Lead Optimization," J.Am. Chem. Soc., 118:1669-1676, 1996
C39	Aita et al., "Analysis of Local Fitness Landscape with a Model of the Rough Mt. Fuji-Type Landscape: Application to Prolyl Endopeptidase and Thermolysin," Biopolymers. Vol. 54, pp. 64-79, Accepted January 14, 2000
C40	Gogos et al., "Assignment of Enzyme Substrate Specificity by Principal Component Analysis of Aligned Protein Sequences: An Experimental Test Using DNA Glycosylase Homologs," Proteins: Structure, Function, and Genetics, 40, pp. 98-105, 2000

Pg. 3 of 8

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure Statement By Applicant	Applicant: Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

 C41	"Vector NTI Suite 7.0 User's Manual (portion) describing software believed to be available prior to February 1, 2000
 	Tobin et al., "Directed Evolution: The 'Rational' Bases for 'Irrational'
C42	
 	Design," Curr. Opin Struct Biol., 10:421-427, 2000
C43	van Regenmortel, M.H., "Are There Two Distinct Research Strategies for
	Developing Biologically Active Molecules: Rational Design and Empirical
	Selection?", J. Mol. Recognit, 13:1-4, 2000
C44	Ryu DD et all, "Recent Progress in Biomolecular Engineering," Biotechnol
	Prog., 16:2-16, 2000
C45	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J.
	Mol. Recognit, 14:308-314, 2001
C46	Glieder et al., "Laboratory Evolution of a Soluble, Self-Sufficient, Highly
	Active Alkaline Hydroxylase," Nat Biotechnol, 20:1135-1139, 2002
C47	Lehman et al., "Exchanging the Active Site Between Phytases for Altering the
-	Functional Properties of the Enzyme," Protein Sci, 9:1866-1872, 2000
C48	Kwasigroch et all, "PoPMuSiC, Rationally Designing Point Mutations in
0.0	Protein Structures," Bioinformatics, 16:1701-1702, 2002
 C49	Tangri et al., "Rationally Engineered Proteins or Antibodies with Absent or
0.5	Reduced Immunogenicity," Curr Med Chem, 9:2191-2199, 2002
 C50	Pierce et al., "Protein Design is NP-Hard," Protein Eng, 15:779-782, 2002
	Ness et al., "Molecular Breeding: The Natural Approach to Protein Design,"
051	Adv Protein Chem, 55:261-292, 2000
 C52	Lehmann et al., "The Consensus Concept for Thermostability Engineering of
052	Proteins: Further Proof of Concept," Protein Eng., 15:403-411, 2002
 C53	Dimmic et al., "rtREV: An Amino Acid Substitution Matrix for Inference of
1033	Retrovirus and Reverse Transcriptase Phylogeny," J. Mol Evol, 55:65-73,
	2002
 C54	
034	Reductase," Protein Eng, 14:633-638, 2001
 C55	Strom et al., "Important Structural Features of 15-Residue Lactoferricin
1 033	
	Derivatives and Methods for Improvement of Antimicrobial Activity,"
 000	Biochem Cell Biol, 80:65-74, 2002
C56	Choulier et al., "QSAR Studies Applied to the Prediction of Antigen-Antibody
 	Interaction Kinetics as Measured by BIACORE," Protein Eng, 15(5):378-382 (20)
C57	Hoover et al., "DNAWorks: An Automated Method for Designing
I	Oligonucleotides for PCR-Based Gene Synthesis, "Nucleic Acids Res,
1	30:E43, 2002

Pg. 4 of 8

Form 1449 (Modified)	Atty Docket No.	Application No.:
	MXGNP004X1/0311.310	10/629,351
Information Disclosure	Applicant:	
Statement By Applicant	Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

C58	Abecassis et all, "High Efficiency Family Shuffling Based on Multi-Step PCR and In vivo DNA Recombination in Yeast: Statistical and Functional Analysis of a Combinatorial Library Between Human Cytochrome P460 1A1 and 1A2," Nucleic Acids Res., 28:E88, 2000
C60	Atta et al., "Surveying a Local Fitness Landscape of a Protein with Epistatic Altee for the Study of Directed Evolution," Biopolymers, 64:95-106, 2002
C61	Prusis et al., "Proteo-chemometrics Analysis of MSH Peptide Binding to Melancortin Receptors," Protein Eng, 15:305-311, 2002
C62	Prusis et al., "PLS Modeling of Chimeric MS04/MSH-Peptide and MCI/MC3-Receptor Interaction Reveals a Novel Method for the Analysis of Ligand-Receptor Interactions," Biochim Biophys Acta, 1544(1-2):350-357, 2001
C63	Lu et al., "Predicting the Reactivity of Proteins from Their Sequence Alone: Kazal Family of Protein Inhibitors of Serine Proteinases," Proc Natl Acad Sci USA, 98(4):1410-1415, 2001
C64	Schein et al., "Chloroplast Transit Peptide Prediction: A Peek Inside the Black Box," Nucleic Acids Res, 29:E82, 2001
C65	Fariselli et al., "Prediction of Protein-Protein Interaction Sites in Heterocomplexes with Neural Networks," Eur J Biochem, 269:1356-1361, 2002
C66	Fariselli et al., "Prediction of Contact Maps with Neural Networks and Correlated Mutations," Protein Eng. 14(11): 835-843, 2001
C67	Marvanova et al., "Biochemical Characterization of Broad-Specificity Enzymes Using Multivariate Experimental Design and a Colorimetric Microplate Assay: Characterization of the Haloalkane Dehalogenase Mutants," J. Microbiol Methods, 44:14-157, 2001
C68	Looger et al., "Computational Design of Receptor and Sensor Proteins with Novel Functions, Nature, 423:185-190, 2003
C69	Govindarajan et al., "Systematic Variation of Amino Acid Substitutions for Stringent Assessment of Pairwise Covariation," J. Mol. Biol, 328:1061-1069, 2003
C70	del Sol Mesa et al., "Automatic Methods for Predicting Functionality Important Residues," J Mol Biol, 326:1289-1302, 2003
C71	Benos et al., "Additivity in Protein-DNA Interactions: How Good an Approximation is it?" Nucleic Acids Res 30(20): 4442-51, 2002
C72	Bogarad et al., "A Hierarchical Approach to Protein Molecular Evolution," Proc Natl Acad Sci USA, 96:2591-2595, 0666 (1999)

Pg. 5 of 8

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure	Applicant:	
Statement By Applicant	Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

C73	Carlsen et al., "QSAR's Based on Partial Order Ranking," SAR QSAR
	Environ Res, 13(1): 153-165, 2002
C74	Crameri et al., "DNA Shuffling of a Family of Genes from Diverse Species
	Accelerates Directed Evolution," Nature, 391:288-291, 1998
C75	Dill K.A., "Additivity Principles in Biochemistry," J Biol Chem, 272(2): 701-704, 1997
C76	Distefano et al., "Quantifying Beta-Sheet Stability by Phage Display," J Mol Biol, 322(1):179-188, 2002
C77	Hayes et al., "Combining Computational and Experimental Screening for Rapid Optimization of Protein Properties," Proc Natl Acad Sci USA, 99(25):15926-15931, 2002
C78	Kell, D.B., "Metabolomics and Machine Learning: Explanatory Analysis of Complex Metabolome Data Using Genetic Programming to Produce Simple, Robust Rules," Mol Biol Rep, 29(1-2): 237-241, 2002
C79	Koshi et al., "Context-Dependent Optimal Substitution Matrices," Protein Eng, 8:641-645, 1995
C80	Koshi et al., "Mutation Matrices and Physical-Chemical Properties: Correlations and Implications," Proteins 27(3):336-344, 1997
C81	Lahr et al., "Patterned Library Analysis: A Method for the Quantitative Assessement of Hypotheses Concerning the Determinants of Protein Structure," Proc Natl Acad Sci USA, 96(26):14860-14865, 1999
C82	Lapinsh et al., "Classification of G-Protein Coupled Receptors by Alignment Independent Extraction of Principal Chemical Properties of Primary Amino Acid Sequences," Protein Sci 11(4):795-805 (2002)
C83	Lapinsh et al., "Development of Proteo-Chemometrics: A Novel Technology for the Analysis of Drug Receptor Interactions," Biochim Biophys Acata, 1325(1-2): 180-190 (2002)
C84	Lapinsh et al., "Protechemometrics Modeling of the Interaction of Amine G- Protein Coupled Receptors with a Diverse Set of Ligands," Mol Pharmacol 61(6): 1465-1475, 2002
C85	Lapinsh et al., "QSAR and Proteo-Chemometric Analysis of the Interaction of a Series of Organic Compounds with Melanocortin Receptor Subtypes," J Med Chem, 46(13): 2572-2579, 2003
C86	Lee et al., "Mathematical Modelling of Inset Neuropeptide Potencies. Are Quantitatively Predictive Models Possible," Insect Biochem Mol Biol, 30(10): 899-907, 2000

Pg. 6 of 8

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure Statement By Applicant	Applicant: Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

C87 Lehman et al., "Engineering Proteins Thermostability: the Use of sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology 12:371-375, 2001 C88 Linusson et al., Statistical Molecular Design of Building Blocks for Combinatorial Chemistry," J Med Chem, 43(7): 1320-1328, 2000 C89 Matsuura eta I., "Nonaddivity of Mutational Effects on the Properties of Catalasa I and its Application to Efficient Directed Evolution," Protein Eng, 11(9): 789-795, 1998 C90 Nakai et al., "Structure Modification and Functionality of Why Proteins: Quantitative Structure-Activity Relationship Approach," J Dairy Sci, 68(10):2763-2772, 1985 C91 Nakai et al., "Recent Advances in Structure and Function of Food Proteins: QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993) C92 Ness et al., "Synthetic Shuffling Expands Functional Protein Diversity by Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Niggemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6: 727-734, 2003 C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 20			
Combinatorial Chemistry." J Med Chem, 43(7): 1320-1328, 2000 C89 Matsuura eta 1., "Nonaddivity of Mutational Effects on the Properties of Catalasa I and its Application to Efficient Directed Evolution," Protein Eng, 11(9): 789-795, 1998 C90 Nakai et al., "Structure Modification and Functionality of Why Proteins: Quantitative Structure-Activity Relationship Approach," J Dairy Sci, 68(10):2763-2772, 1985 C91 Nakai et al., "Secent Advances in Structure and Function of Food Proteins: QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993) C92 Ness et al., "Synthetic Shuffling Expands Functional Protein Diversity by Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Niggemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6:727-734, 2003 C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function Properties from Amino Acid Composition," J Agric Food Chem, 49(2): 831-885, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C87	
Catalasa I and its Application to Efficient Directed Evolution," Protein Eng, 11(9): 789-795, 1998 C90 Nakai et al., "Structure Modification and Functionality of Why Proteins: Quantitative Structure-Activity Relationship Approach," J Dairy Sci, 68(10):2763-2772, 1985 C91 Nakai et al., "Recent Advances in Structure and Function of Food Proteins: QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993) C92 Ness et al., "Synthetic Shuffling Expands Functional Protein Diversity by Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Nigemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003) C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled	•	C88	Combinatorial Chemistry," J Med Chem, 43(7): 1320-1328, 2000
Quantitative Structure-Activity Relationship Approach," J Dairy Sci, 68(10):2763-2772, 1985 C91 Nakai et al., "Recent Advances in Structure and Function of Food Proteins: QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993) C92 Ness et al., "Synthetic Shuffling Expands Functional Protein Diversity by Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Niggemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003) C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function Properties from Amino Acid Composition," J Agric Food Chem, \$1(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C89	Catalasa I and its Application to Efficient Directed Evolution," Protein Eng,
QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993) C92 Ness et al., "Synthetic Shuffling Expands Functional Protein Diversity by Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Niggemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003) C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C90	Quantitative Structure-Activity Relationship Approach," J Dairy Sci,
Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002 C93 Niggemann et al., "Exploring Local and Non-Local Interactions for Protein Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6: 727-734, 2003 C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C91	QSAR Approach," Crit Rev Food Sci Nutr, 33(6):477-499 (1993)
Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000 C94 Nikolova et al., "Semirational Design of Active Tumor Suppressor p53 DNA Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003) C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C92	Allowing Amino Acids to Recombine Independently," Nat Biotechnol, 20(12):1251-1255, 2002
Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25): 14675-14680, 1998 C95 Reymond et al., "Substrate Arrays as Enzyme Fingerprinting Tools," Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6: 727-734, 2003 C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled	(C93	Stability by Structural Motif Engineering," J Mol Biol, 296(1):181-195, 2000
Chembiochem, 3(8):701-708, 2002 C100 Sadowski et al., "Automated Generation and Refinement of Protein Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003) C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C94	Binding Domain with Enhanced Stability," Proc Natl Acad Sci USA, 95(25):
Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6): 727-734, 2003 C101 Shaw et al., "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled	1	C95	Chembiochem, 3(8):701-708, 2002
Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-300, 2002 C102 Sheridan et al., "Designing Targeted Libraries with Genetic Algorithms," J Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		2100	Signatures: Case Study with G-Protein Coupled Receptors," Bioinformatics, 19(6(: 727-734, 2003
Mol Graph Model, 18(4-5): 320-345, 525, 2000 C103 Siebert, K.J., "Quantitative Structure-Activity Relationship Modeling of Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		2101	Specificity Solely from Protein Sequences," Biotechnol Bioeng, 79(3): 295-
Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001 C104 Siebert, K.J., "Modeling Protein Function Properties from Amino Acid Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled	C	C102	Mol Graph Model, 18(4-5): 320-345, 525, 2000
Composition," J Agric Food Chem, 51(26): 7792-7797, 2003 C105 Soyer et al., "Using Evolutionary Methods to Study G-Protein Coupled		C103	Peptide and Protein Behavior as a Function of Amino Acid Composition," J Agric Food Chem, 49(2): 851-858, 2001
			Composition," J Agric Food Chem, 51(26): 7792-7797, 2003
		2105	

Pg. 7 of 8

Form 1449 (Modified)	Atty Docket No. MXGNP004X1/0311.310	Application No.: 10/629,351
Information Disclosure Statement By Applicant	Applicant: Gustafsson et al.	
	Filing Date	Group
(Use Several Sheets if Necessary)	July 29, 2003	1645

	C106	Steipe, B., "Evolutionary Approaches to Protein Engineering," Curr Top Microbiol Immunol, 243: 55-86, 1999			
	C107	Umeno et al., "Evolution of the C30 Carotenoid Synthase CrtM for Function			
		in a C40 Pathway," J Bacteriold 184(23): 6690-6699, 2002			
	C108	Veraverbeke et al., "Wheat Protein Composition and Properties of Wheat			
			dmaking Functionality," Crit Rev Food Sci Nutr,		
		42(3): 179-208, 2002			
	C109	Wahler et al., "Enzyme Fingerprints by Fluorogenic and Chromogenic			
		Substrate Arrays," Angew Chem Int Ed Engl., 40(23): 4457-4460, 2001			
	C110	Wahler et al., "Enzyme Fingerprints of Activity, and Stereo and			
1		Enantioselectivity from Fluorogenic and Chromogenic Substrate Arrays,"			
		Chemistry, 8(14): 3211-3228, 2002			
	C111	Wang et al., "Designing Gene Libraries from Protein Profiles for			
		Combinatorial Protein Experiments," Nucleic Acids Res, 30(21): e120, 2002			
	C112	Wells, J.A., "Additivity of Mutational Effects in Proteins," Biochemistry,			
		29(37): 8509-8517, 1990			
	C113	Wikberg et al., "Melanocortin Receptors: Ligands and Protechemometrics			
		Modeling," Ann NY Acad Sci, 994:21-26, 2003			
	C114	Martin et al., "Measuring Diversity: Experimental Design of Combinatorial			
		Libraries for Drug Discovery," J. Med. Chem. 38, 1431-1436, 1995			
	C115	Sheridan et al., "Using a Genetic Algorithm to Suggest Combinatorial Libraries," J. Chem. Inf. Compu. Sci., 35, 310-320, 1995			
	C116	D.K. Agrafiotis, "Multiobjective Optimization of Combinatorial Libraries,"			
		IBM J. Res & Dev., Vol, 45, No. 3, 545-566, 2001			
Examiner			Date Considered		
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00/10/2010					

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